

Snapshot: Chromatin Remodeling Complexes

Cell

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INO80								
Subfamily	INO80			SWR1				
Species	Yeast	Fly	Human	Yeast	Human	Fly	Human	Yeast
Complex	INO80	Pho-dINO80	INO80	SWR1	SRCAP	Tip60	TRRAP/Tip60	NuA4
Homologous subunits ^a	Ino80	dIno80	hIno80	Swr1	SRCAP	Domino	P400	
	Rvb1, Rvb2	Reptin, Pontin	Tip49a, Tip49b	Rvb1, Rvb2	Tip49a, Tip49b	Reptin, Pontin	Tip49a, Tip49b	
	Arp4,5,8, Act1	dArp5,8, dActin	BAF53a, Arp5,8	Arp4,6, Act1	BAF53a, Arp6	BAP55, Act87E	BAF53a, Actin	Arp4, Act1
	Taf14			Yaf9	GAS41	dGAS41	GAS41	Yaf9
	Ies2		hIes2					
	Ies6		hIes6					
				Swc4/Eaf2	DMAP1	dDMAP1	DMAP1	Swc4/Eaf2
Unique subunits				Swc2/Vps72	YL-1	dYL-1	YL-1	
				Bdf1		dBrd8	Brd8/TRCP120	
				H2AZ, H2B	H2AZ, H2B	H2Av, H2B		
				Swc6/Vps71	ZnF-HIT1			
						dTra1	TRRAP	Tra1
						dTIP60	Tip60	Esa1
						dMRG15	MRG15, MRGX	Eaf3
Unique subunits	Ies1, Ies3-5, Nhp10	Pho	Amida, NFRKB, MCRS1, FLJ90652, FLJ20309	Swc3,5,7		E(Pc)	EPC1, EPC-like	Epl1
						dING3	ING3	Yng2
								Eaf5, Eaf1/ Vid21

• INO80 regulates transcription and is involved in DNA repair and cell-cycle checkpoint adaptation. It has ATP-dependent nucleosome mobilization activity in vitro.

• SWR1 regulates transcription and is also involved in deposition of histone H2AZ, chromosome stability, and cell-cycle checkpoint adaptation. In vitro it can replace pre-existing nucleosomal H2A-H2B dimers with H2AZ-H2B dimers in an ATP-dependent manner.

• NuA4 acetylates histone H4 tails and regulates transcription, cell-cycle progression, and DNA repair; in vitro it also acetylates histone H2A. In higher organisms, TIP60 may integrate both NuA4 and SWR1 functions regulating transcription, the DNA-damage response, cellular growth control, and apoptosis.

ISWI							
Subfamily	ACF/CHRAC					NURF	
Species	Yeast	Yeast	Yeast	Fly	Human	Fly	Human
Complex	ISW1a	ISW1b	ISW2 ^b	ACF ^c	ACF ^d	NURF	NURF
Homologous subunits ^a	Isw1	Isw1	Isw2	ISWI	hSNF2H	ISWI	hSNF2L
			Itc1	ACF1	WCRF180/hACF1	NURF301	BPTF
						NURF55/p55	RbAP46, RbAP48
Unique subunits	Ioc3	Ioc2, Ioc4				NURF38	

• ACF and CHRAC are involved in transcription, DNA replication through heterochromatin, and proper chromatin assembly. *Drosophila* CHRAC promotes replication initiation; in vitro ACF interacts with naked DNA and nucleosomal arrays independent of ATP, assembling nucleosomes into regularly spaced chromatin.

• NURF regulates expression of homeotic genes, modulates Wnt-signaling, and affects higher-order chromatin structure; in vitro NURF catalyzes formation of regularly spaced nucleosomal arrays and facilitates transcription activation.

Mi-2/CHD					
Subfamily	CHD1			Mi-2/CHD	
Species	Yeast	Fly	Human	Fly	Human
Complex	CHD1	CHD1	CHD1	Mi-2/ NuRD	NuRD ^a
Homologous subunits ^a	Chd1	dCHD1	CHD1	dMi-2	Mi-2 α /CHD3, Mi-2 β /CHD4
				dMBD2/3	MBD3
				dMTA	MTA1,2,3
				dRPD3	HDAC1,2
				p55	RbAp46,48
Unique subunits				p66/68	p66 α , β
					DOC-1?

• CHD1 promotes transcription elongation; in vitro it promotes the formation of regularly spaced nucleosomal arrays.

• Mi-2/CHD deacetylates chromatin, represses transcription, and regulates development; in vitro Mi-2/CHD also promotes nucleosome sliding.

• Yeast SWI/SNF regulates transcription, mitotic exit, and activation of weak replication origins. In vitro it binds hyperacetylated nucleosomes, mobilizes nucleosomes, and acts as a directional DNA translocase. Yeast RSC is involved in transcription, sister chromatid cohesion, chromosome segregation, and cell-cycle progression. RSC and SWI/SNF play distinct roles in DNA repair.

• *Drosophila* BAP activates transcription, promotes homeotic gene expression, and is involved in chromatin assembly and mitosis.

• Human BAF regulates gene expression, cell-cycle progression, organ development, and immune responses. In vitro, human BAF disrupts tailless nucleosomes. BAP and BAF contain conventional actin, similar to INO80 and SWR1.

SWI/SNF				
Subfamily	SWI/SNF			
Species	Yeast	Yeast	Fly	Human
Complex	SWI/SNF	RSC	BAP ^a	BAF ⁱ
Homologous subunits ^a	Swi2/ Snf2	Sth1	BRM	BRG1 or hBRM
	Swi1/ Atr6		OSA/ eyelid	BAF250/ hOSA1
		Rsc1 or Rsc2, Rsc4		
	Swi3	Rsc8	MOR/ BAP155	BAF155, BAF170
	Swp73	Rsc6	BAP60	BAF60a
	Arp7, Arp9	Arp7, Arp9	BAP55, BAP47	BAF53
	Snf5	Sth1	SNR1/ BAP45	hSNF5
			BAP111/ dalao	BAF57
			β -actin	β -actin
	Swp82, Taf14, Snf6, Snf11	Rsc3,5,7,9, 10,30, Htt1, Ldb7, and Rtt102		
Unique subunits				

Footnotes

^aFirst row indicates core ATPase.

^bA variant ISW12 complex also contains Dis1 and Dpb4 in addition to Isw2 and Itc1.

^c*Drosophila* CHARC also contains CHARC14/p14, CHARC16/p16 in addition to ISWI and ACF1.

^dHuman CHARC also contains hCHARC15, hCHARC17 in addition to hSNF2H and hACF1. hSNF2H has also been found in other human ISWI complexes: RSF, WICH, B-WICH, and SNF2h/NuRD/cohesion complexes.

^ePBAP complex contains Polyromo and BAP170 rather than OSA.

^fPBAF complex contains BAF180 and BAF200 rather than BAF250.

^gHuman MeCP1 complex contains MBD2 instead of MBD3; MEP50 and PRMT5 are also found in human MeCP1.

SnapShot: Chromatin Remodeling Complexes

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Abbreviations

SWI/SNF: switching/sucrose nonfermenting
RSC: remodels the structure of chromatin
BAP: Brahma-associated proteins
PBAP: Polybromo-associated BAP
BAF: BRG1- or hBRM-associated factors
PBAF: Polybromo-associated BAF
INO80: inositol requiring
SWR1: Sick with Rat8 ts
NuA4: nucleosome acetyltransferase of H4
TIP60: Tat-interactive protein 60 kDa
SRCAP: Snf2-related CREB binding protein activator protein
TRRAP: transformation/transcription domain associated protein
ISWI: imitation switch
ACF: ATP-utilizing chromatin assembly and remodeling factor
CHRAc: chromatin-accessibility complex
NURF: nucleosome remodeling factor
CHD: chromo-helicase/ATPase DNA binding
NuRD: nucleosome remodeling histone deacetylase

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REFERENCES

- Bao, Y., and Shen, X. (2007). INO80 subfamily of chromatin remodeling complexes. *Mut. Res.* 618, 18–29.
- Becker, P.B., and Horz, W. (2002). ATP-dependent nucleosome remodeling. *Annu. Rev. Biochem.* 71, 247–273.
- Bouazoune, K., and Brehm, A. (2006). ATP-dependent chromatin remodeling complexes in *Drosophila*. *Chromosome Res.* 14, 433–449.
- Bowen, N.J., Fujita, N., Kajita, M., and Wade, P.A. (2004). Mi-2/NuRD: multiple complexes for many purposes. *Biochim. Biophys. Acta* 1677, 52–57.
- Cairns, B.R. (2005). Chromatin remodeling complexes: strength in diversity, precision through specialization. *Curr. Opin. Genet. Dev.* 15, 185–190.
- Chi, T. (2004). A BAF-centred view of the immune system. *Nat. Rev. Immunol.* 4, 965–977.
- Corona, D.F., and Tamkun, J.W. (2004). Multiple roles for ISWI in transcription, chromosome organization and DNA replication. *Biochim. Biophys. Acta* 1677, 113–119.
- Doyon, Y., and Cote, J. (2004). The highly conserved and multifunctional NuA4 HAT complex. *Curr. Opin. Genet. Dev.* 14, 147–154.
- Eberharter, A., and Becker, P.B. (2004). ATP-dependent nucleosome remodelling: factors and functions. *J. Cell Sci.* 117, 3707–3711.
- Kornberg, R.D., and Lorch, Y. (1999). Chromatin-modifying and -remodeling complexes. *Curr. Opin. Genet. Dev.* 9, 148–151.
- Le Guezennec, X., Vermeulen, M., Brinkman, A.B., Hoeijmakers, W.A., Cohen, A., Lasonder, E., and Stunnenberg, H.G. (2006). MBD2/NuRD and MBD3/NuRD, two distinct complexes with different biochemical and functional properties. *Mol. Cell. Biol.* 26, 843–851.
- Lusser, A., Urwin, D.L., and Kadonaga, J.T. (2005). Distinct activities of CHD1 and ACF in ATP-dependent chromatin assembly. *Nat. Struct. Mol. Biol.* 12, 160–166.
- Mellor, J., and Morillon, A. (2004). ISWI complexes in *Saccharomyces cerevisiae*. *Biochim. Biophys. Acta* 1677, 100–112.
- Moshkin, Y.M., Mohrmann, L., van Ijcken, W.F., and Verrijzer, C.P. (2006). Functional differentiation of SWI/SNF remodelers in transcription and cell cycle control. *Mol. Cell Biol.* 27, 651–661.
- Narlikar, G.J., Fan, H.Y., and Kingston, R.E. (2002). Cooperation between complexes that regulate chromatin structure and transcription. *Cell* 108, 475–487.
- Olave, I.A., Reck-Peterson, S.L., and Crabtree, G.R. (2002). Nuclear actin and actin-related proteins in chromatin remodeling. *Annu. Rev. Biochem.* 71, 755–781.
- Smith, C.L., and Peterson, C.L. (2005). ATP-dependent chromatin remodeling. *Curr. Top. Dev. Biol.* 65, 115–148.
- Tsukiyama, T. (2002). The in vivo functions of ATP-dependent chromatin-remodelling factors. *Nat. Rev. Mol. Cell Biol.* 3, 422–429.
- Tsukiyama, T., and Wu, C. (1997). Chromatin remodelling and transcription. *Curr. Opin. Genet. Dev.* 7, 182–191.
- Yan, Z., Cui, K., Murray, D.M., Ling, C., Xue, Y., Gerstein, A., Parsons, R., Zhao, K., and Wang, W. (2005). PBAF chromatin-remodeling complex requires a novel specificity subunit, BAF200, to regulate expression of selective interferon-responsive genes. *Genes Dev.* 19, 1662–1667.